

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-11 (canceled)

12. (New): A method for evaluating a human for being at risk for a VCAM-1 ligand mediated disease, the method comprising:

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2;

(b) identifying a single nucleotide polymorphism (SNP) at at least one of the one or more positions, wherein the polymorphism(s) is/are selected from the group consisting of

a C at position 278,

a G at position 647,

a C at position 707,

a C at position 748,

an A at position 829, and

a C at position 1467; and

(c) diagnosing the human as being at risk for a VCAM-1 ligand mediated disease.

13. (New): The method of claim 12, wherein the nucleic acid sample comprises a fragment of a VCAM-1 nucleic acid.

14. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is multiple sclerosis.

15. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is rheumatoid arthritis.

16. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is atherosclerosis.

17. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is allergic asthma.

18. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is inflammatory bowel disease.

19. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is contact dermatitis.

20. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is insulin-dependent diabetes.

21. (New): The method of claim 12, wherein the VCAM-1 ligand mediated disease is glomerulonephritis.

22. (New): The method of claim 12, wherein the human is diagnosed as having or being at risk for having a transplant rejection.

23. (New): The method of claim 12, wherein step (b) comprises performing an ARMSTM assay, ALEXTM assay, COPS assay, TaqmanTM assay, Molecular Beacons assay, RFLP assay, restriction site based PCR, or a FRET technique.

24. (New): The method of claim 12, wherein a C is identified at position 278.
25. (New): The method of claim 12, wherein a G is identified at position 647.
26. (New): The method of claim 12, wherein a C is identified at position 707.
27. (New): The method of claim 12, wherein a C is identified at position 748.
28. (New): The method of claim 12, wherein an A is identified at position 829.
29. (New): The method of claim 12, wherein a C is identified at position 1467.
30. (New): The method of claim 12, wherein the sample is tested to determine the identities of the nucleotides at at least two of the positions.
31. (New): The method of claim 12, wherein the sample is tested to determine the identities of the nucleotides at all six of the positions.
32. (New): An allele-specific primer that specifically detects one or more polymorphisms in a VCAM-1 nucleic acid, wherein the polymorphisms are at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2.
33. (New): The primer of claim 32, wherein the polymorphic position of the primer is within 6-8 nucleotides of the 3' end of the primer.
34. (New): The primer of claim 32, wherein the primer is 17-50 nucleotides long.

35. (New): The primer of claim 32, wherein the primer is 17-35 nucleotides long.
36. (New): The primer of claim 32, wherein the primer is 17-30 nucleotides long.
37. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 278 of SEQ ID NO:2.
38. (New): The primer of claim 32, wherein the primer distinguishes between a C and a T at position 278 of SEQ ID NO:2.
39. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 647 of SEQ ID NO:2.
40. (New): The primer of claim 32, wherein the primer distinguishes between a G and an A at position 647 of SEQ ID NO:2.
41. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 707 of SEQ ID NO:2.
42. (New): The primer of claim 32, wherein the primer distinguishes between a C and a T at position 707 of SEQ ID NO:2.
43. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 748 of SEQ ID NO:2.
44. (New): The primer of claim 32, wherein the primer distinguishes between a C and a T at position 748 of SEQ ID NO:2.

45. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 829 of SEQ ID NO:2.

46. (New): The primer of claim 32, wherein the primer distinguishes between an A and a G at position 829 of SEQ ID NO:2.

47. (New): The primer of claim 32, wherein the primer specifically detects a polymorphism at position 1467 of SEQ ID NO:2.

48. (New): The primer of claim 32, wherein the primer distinguishes between a C and a T at position 1467 of SEQ ID NO:2.

49. (New): An allele-specific oligonucleotide probe that specifically detects one or more polymorphisms in a VCAM-1 nucleic acid, wherein the polymorphisms are at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2.

50. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 278 of SEQ ID NO:2.

51. (New): The probe of claim 49, wherein the probe distinguishes between a C and a T at position 278 of SEQ ID NO:2.

52. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 647 of SEQ ID NO:2.

53. (New): The probe of claim 49, wherein the probe distinguishes between a G and an A at position 647 of SEQ ID NO:2.

54. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 707 of SEQ ID NO:2.

55. (New): The probe of claim 49, wherein the probe distinguishes between a C and a T at position 707 of SEQ ID NO:2.

56. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 748 of SEQ ID NO:2.

57. (New): The probe of claim 49, wherein the probe distinguishes between a C and a T at position 748 of SEQ ID NO:2.

58. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 829 of SEQ ID NO:2.

59. (New): The probe of claim 49, wherein the probe distinguishes between an A and a G at position 829 of SEQ ID NO:2.

60. (New): The probe of claim 49, wherein the probe specifically detects a polymorphism at position 1467 of SEQ ID NO:2.

61. (New): The probe of claim 49, wherein the probe distinguishes between a C and a T at position 1467 of SEQ ID NO:2.

62. (New): The probe of claim 49, wherein the probe comprises a detectable label.

63. (New): The probe of claim 49, wherein the probe is 8-50 nucleotides long.

64. (New): The probe of claim 49, wherein the probe is 8-25 nucleotides long.

65. (New): The probe of claim 49, wherein the probe is 8-15 nucleotides long.

66. (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in a VCAM-1 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for having a VCAM-1 ligand mediated disease, wherein the sample comprises a nucleotide at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2; and

(b) testing the sample to determine the identity of at least one of the nucleotides at the one or more positions.

67. (New): The method of claim 66, wherein the nucleic acid sample comprises a fragment of a VCAM-1 nucleic acid.

68. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is multiple sclerosis.

69. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is rheumatoid arthritis.

70. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is atherosclerosis.

71. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is allergic asthma.

72. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is inflammatory bowel disease.

73. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is contact dermatitis.

74. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is insulin-dependent diabetes.

75. (New): The method of claim 66, wherein the VCAM-1 ligand mediated disease is glomerulonephritis.

76. (New): The method of claim 66, wherein the human is diagnosed as having or at risk for having a transplant rejection.

77. (New): The method of claim 66, wherein step (b) comprises performing an ARMSTM assay, ALEXTM assay, COPS assay, TaqmanTM assay, Molecular Beacons assay, RFLP assay, restriction site based PCR, or a FRET technique.

78. (New): The method of claim 66, the method comprising determining that the nucleotide at position 278 is a C.

79. (New): The method of claim 66, the method comprising determining that the nucleotide at position 647 is a G.

80. (New): The method of claim 66, the method comprising determining that the nucleotide at position 707 is a C.

81. (New): The method of claim 66, the method comprising determining that the nucleotide at position 748 is a C.

82. (New): The method of claim 66, the method comprising determining that the nucleotide at position 829 is an A.

83. (New): The method of claim 66, the method comprising determining that the nucleotide at position 1467 is a C.

84. (New): The method of claim 66, the method comprising determining that the nucleotide at position 278 is not a T.

85. (New): The method of claim 66, the method comprising determining that the nucleotide at position 647 is not an A.

86. (New): The method of claim 66, the method comprising determining that the nucleotide at position 707 is not a T.

87. (New): The method of claim 66, the method comprising determining that the nucleotide at position 748 is not a T.

88. (New): The method of claim 66, the method comprising determining that the nucleotide at position 829 is not an G.

89. (New): The method of claim 66, the method comprising determining that the nucleotide at position 1467 is not a T.

90. (New): The method of claim 66, wherein the identities of at least two of the nucleotides are determined.

91. (New): The method of claim 66, wherein the identities of all six of the nucleotides are determined.

92. (New): A method for characterizing the genotype of a human diagnosed as having or at risk for having a VCAM-1 ligand mediated disease, the method comprising:

(a) providing a nucleic acid sample from the human, wherein the sample comprises a nucleotide at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2;

(b) testing the sample to determine the identity of at least one of the nucleotide(s); and

(c) recording the identity of the at least one nucleotide in a print or computer-readable medium.

93. (New): The method of claim 92, wherein the nucleic acid sample comprises a fragment of a VCAM-1 nucleic acid.

94. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is multiple sclerosis.

95. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is rheumatoid arthritis.

96. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is atherosclerosis.

97. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is allergic asthma.

98. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is inflammatory bowel disease.

99. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is contact dermatitis.

100. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is insulin-dependent diabetes.

101. (New): The method of claim 92, wherein the VCAM-1 ligand mediated disease is glomerulonephritis.

102. (New): The method of claim 92, wherein the human is diagnosed as having or at risk for having a transplant rejection.

103. (New): The method of claim 92, wherein step (b) comprises performing an ARMSTM assay, ALEXTM assay, COPS assay, TaqmanTM assay, Molecular Beacons assay, RFLP assay, restriction site based PCR, or a FRET technique.

104. (New): The method of claim 92, the method comprising determining that the nucleotide at position 278 is a C.

105. (New): The method of claim 92, the method comprising determining that the nucleotide at position 647 is a G.

106. (New): The method of claim 92, the method comprising determining that the nucleotide at position 707 is a C.

107. (New): The method of claim 92, the method comprising determining that the nucleotide at position 748 is a C.

108. (New): The method of claim 92, the method comprising determining that the nucleotide at position 829 is an A.

109. (New): The method of claim 92, the method comprising determining that the nucleotide at position 1467 is a C.

110. (New): The method of claim 92, the method comprising determining that the nucleotide at position 278 is not a T.

111. (New): The method of claim 92, the method comprising determining that the nucleotide at position 647 is not an A.

112. (New): The method of claim 92, the method comprising determining that the nucleotide at position 707 is not a T.

113. (New): The method of claim 92, the method comprising determining that the nucleotide at position 748 is not a T.

114. (New): The method of claim 92, the method comprising determining that the nucleotide at position 829 is not a G.

115. (New): The method of claim 92, the method comprising determining that the nucleotide at position 1467 is not a T.

116. (New): The method of claim 92, wherein the identities of at least two of the nucleotides are determined and recorded.

117. (New): The method of claim 92, wherein the identities of all six of the nucleotides are determined and recorded.

118. (New): A method for characterizing the genotype of a human diagnosed as having or at risk for having a disorder selected from the group consisting of multiple sclerosis, atherosclerosis, allergic asthma, inflammatory bowel disease, contact dermatitis, insulin-dependent diabetes, and glomerulonephritis, wherein the method comprises:

(a) providing a nucleic acid sample from the human, wherein the sample comprises a nucleotide at one or more of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2;

(b) testing the sample to determine the identity of at least one of the nucleotides at the one or more positions; and

(c) recording the identity of the at least one nucleotide in a print or computer-readable medium.

119. (New): A method for characterizing the genotype of a human diagnosed as having or at risk for having a VCAM-1 ligand mediated disease, the method comprising:

(a) providing a nucleic acid sample from the human, wherein the sample comprises a nucleotide at each of the positions corresponding to positions 278, 647, 707, 748, 829, and 1467 of SEQ ID NO:2;

(b) testing the sample to determine the identities of the nucleotides at all six of the positions; and

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(c) recording the identities of the six nucleotides in a print or computer-readable medium.